Figure 1

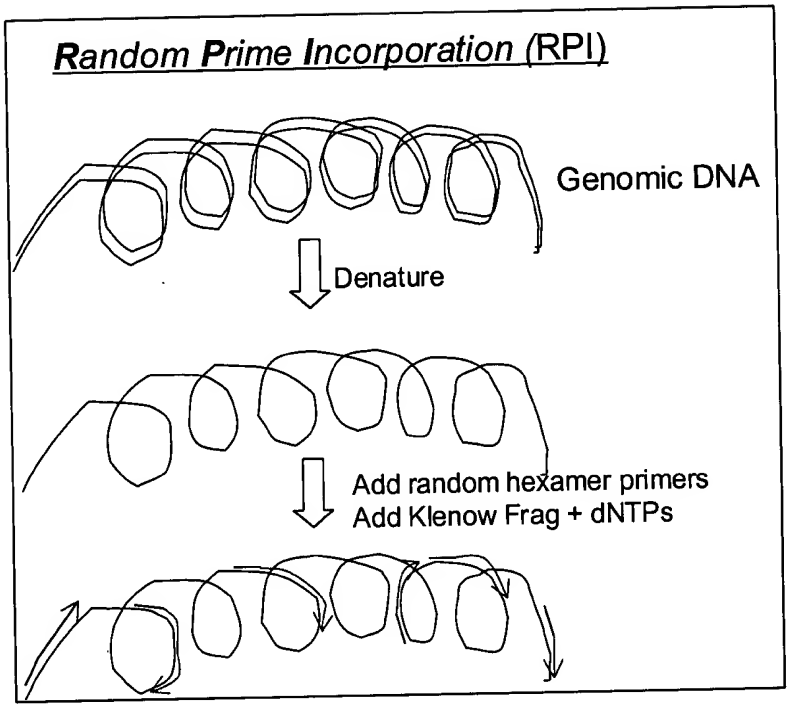

Random Prime Incorporation (RPI)
Genomic DNA
Denature
Add random hexamer primers
Add Klenow Frag + dNTPs

Figure 2

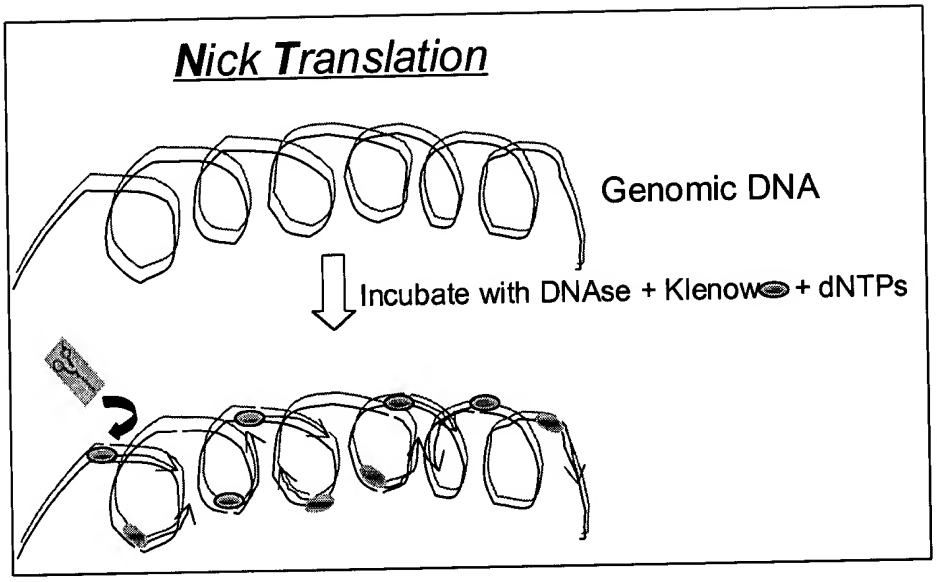

Nick Translation
Genomic DNA
Incubate with DNAse + Klenow + dNTPs

Figure 3

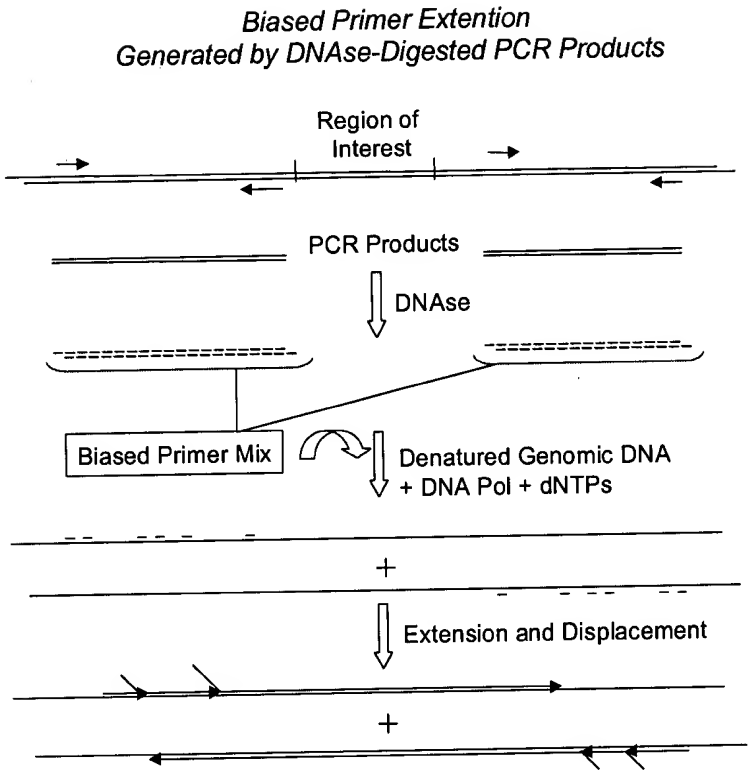

Biased Primer Extention
Generated by DNAse-Digested PCR Products
Region of
Interest
PCR Products
DNAse
Biased Primer Mix
Denatured Genomic DNA
+ DNA Pol + dNTPs
+
Extension and Displacement
+

Figure 4

Gene-Specific Primer Extension using DNA Polymerase

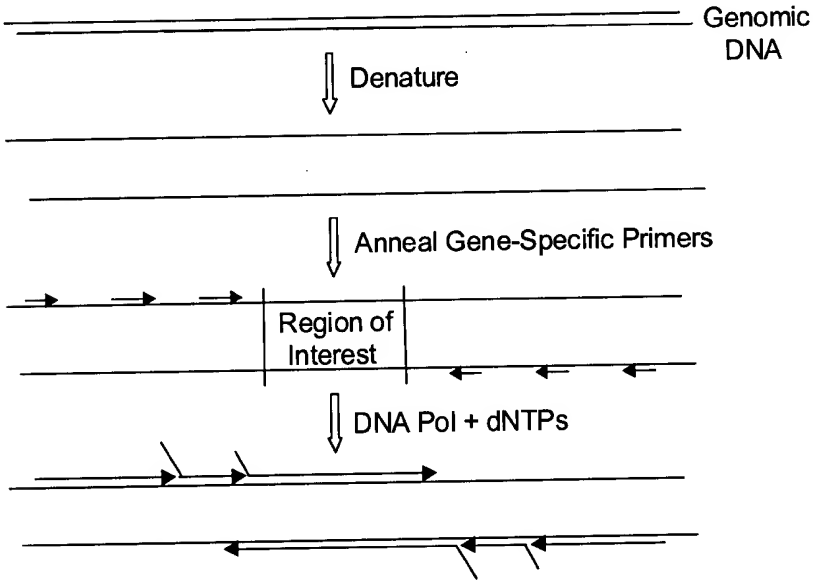


Figure 5

Extension Displacement Transcription Incorporation (EDTI)

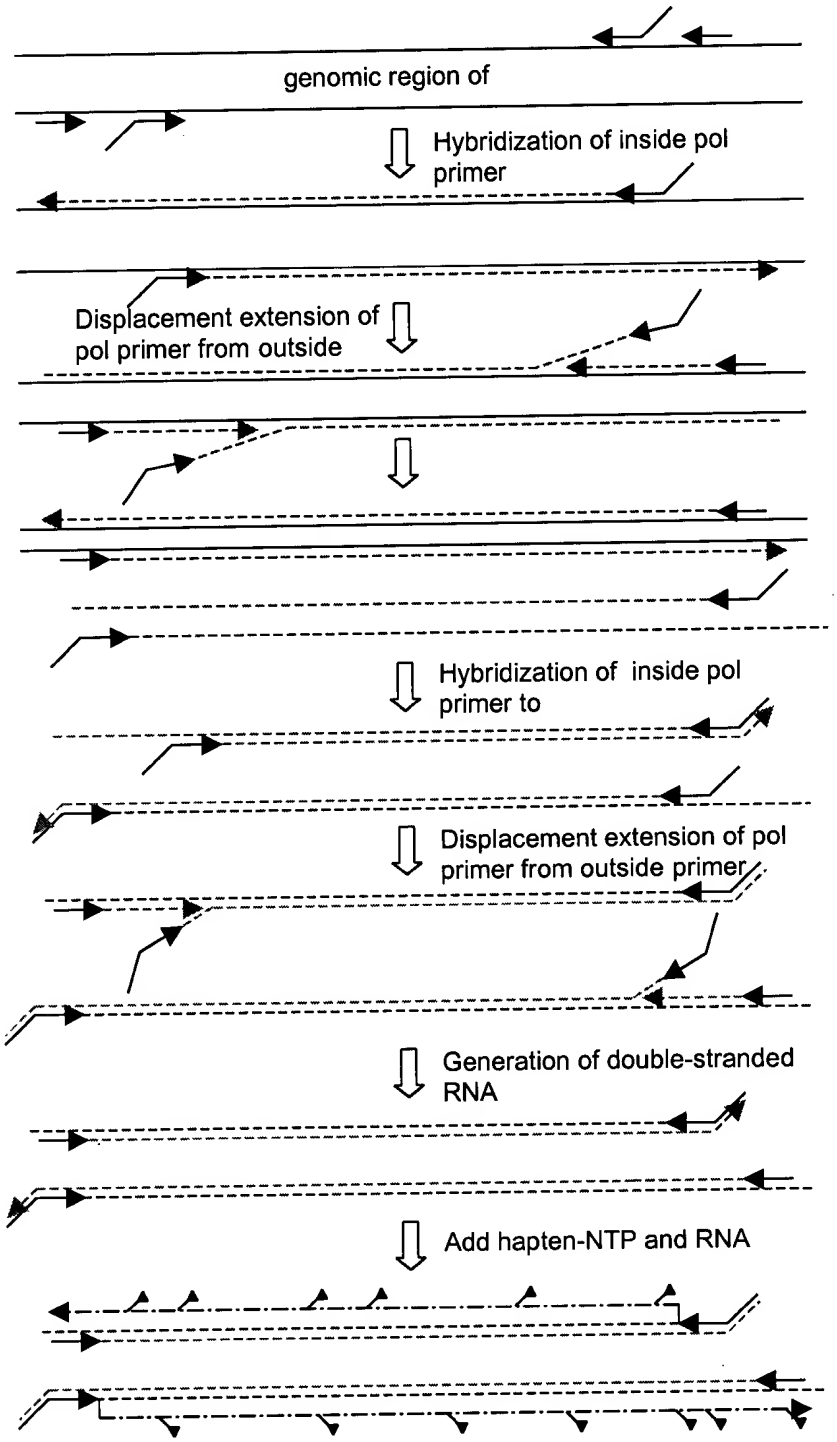


Figure 6

1. 'A' Allele, CYP2D6*3, A_{2637} deletion, Frame[redacted]esulting in zero enzyme activity

2637

5'- G C T A A C T G A G C A C A G G A T G A C C -3' NH2 CYPwt(+)A2624,22mer,54%GC, Tm=63-64C
5'- G C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2 CYPwt(+)A2624(A)30-3'NH2
5'- C T A A C T G A G C A C A G G A T G A C C (A)30-3' NH2 CYPwt(+)A2625(A)30-3'NH2
5'- C T A A C T G A G C A C A G G A T G A C (A)30-3' NH2 CYPwt(+)A2625b(A)30-3'NH2
5'- G C T A A C T G A G C A C - G G A T G A C C -3' NH2 CYPmut(+)A2624,21mer,57%GC, Tm=61-63C
5'- G C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2 CYPmut(+)A2624(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A C C (A)30-3' NH2 CYPmut(+)A2625(A)30-3'NH2
5'- C T A A C T G A G C A C - G G A T G A C (A)30-3' NH2 CYPmut(+)A2625b(A)30-3'NH2

|-2612
5'- G C T G G A T G A G C T G C T A A C T G A G C A C A G G A T G A C C T G G G A C C C A G C C C A G C C -3' Wild Type (+)
5'- G C T G G A T G A G C T G C T A A C T G A G C A C - G G A T G A C C T G G G A C C C A G C C C A G C C -3' Mut (+)

2. 'B' Allele, CYP2D6*4, $G_{1934}A$, Spliceing defect resulting in zero enzyme activity

A. wt Probe - CYPwt(-)B1922 (C/A to mut at base 5) & CYPmut(+)B1922 (A/C to mut at base 13)

1934

NH2 3'- G A G G G T G G G G G T **C** C T G C -5' CYPwt(-)B1922,17mer,76%GC, Tm=66C
5'- C T C C C A C C C C C A G G A C G -3' NH2 CYPwt(+)B1922- Target
5'- C T C C C A C C C C C A A G A C G -3' NH2 CYPmut(+)B1922,17mer,71%GC, Tm=58-60C
NH2 3'- G A G G G T G G G G G T T C T G C -5' CYPmut(-)B1922- Target

|-1909
5'- C C C T T A C C C G C A T C T C C C A C C C C C A G G A C G C C C C T T T C G C C C C A A C G G T C T -3' Wild Type (+)
5'- C C C T T A C C C G C A T C T C C C A C C C C C A A G A C G C C C C T T T C G C C C C A A C G G T C T -3' Mut (+)

B. CYPwt(-)B1930 (C/A to mut at base 13) and CYPmut(+)B1930 (A/C to wt at base 5)

NH2 3'- G G G T **C** C T G C G G G G A A A G -5' CYPwt(-)B1930,17mer,71%GC, Tm=56C
NH2 3'-(A)30 G G G T **C** C T G C G G G G A A A G -5' CYPwt(-)B1930(A)30-3'NH2
5'- C C C A A G A C G C C C C T T T C -3' NH2 CYPmut(+)B1930,17mer,65%GC, Tm=54C
5'- C C C A A G A C G C C C C T T T C (A)30-3' NH2 CYPmut(+)B1930(A)30-3'NH2

|-1909
5'- C C C T T A C C C G C A T C T C C C A C C C C C A G G A C G C C C C T T T C G C C C C A A C G G T C T -3' Wild Type (+)
5'- C C C T T A C C C G C A T C T C C C A C C C C C A A G A C G C C C C T T T C G C C C C A A C G G T C T -3' Mut (+)

3. 'C' Allele, CYP2D6*9, G_{2702}-A_{2704} deletion, decreased enzyme activity

|-2702

5'- G C A G A G A T G G A G A A G G T G A G A G -3' NH2 CYPwt(+)C2691,22mer,55%GC, Tm=60C
5'- G C A G A G A T G G A G A A G G T G A G A G (A)30-3' NH2 CYPwt(+)C2691(A)30-3'NH2
5'- C A G A G A T G G A G A A G G T G A G A G (A)30-3' NH2 CYPwt(+)C2692(A)30-3'NH2
5'- G C A G A G A T G G A - - - G G T G A G A G T G -3' NH2 CYPmut(+)C2691,21mer,57%GC, Tm=60C
5'- G C A G A G A T G G A - - - G G T G A G A G T G (A)30-3' NH2 CYPmut(+)C2691(A)30-3'NH2
5'- C A G A G A T G G A - - - G G T G A G A G T G (A)30-3' NH2 CYPmut(+)C2692(A)30-3'NH2

|-2676
3'- T G A C T C C G G A A G G A C C G T C T C T A C C T **C** T T C C A C T C T C A C C G A C G G T G C C A C -5' Wild Type (-)
3'- T G A C T C C G G A A G G A C C G T C T C T A C C T - - - C C A C T C T C A C C G A C G G T G C C A C -5' Mut (-)

4. 'E' Allele, CYP2D6*7, $A_{3023}C$, $H_{324}P$ amino acid change results in zero enzyme activity

A. wt Probe - CYPwt(-)E3009 (T/C to mut at base 5) & CYPmut(+)E3009 (C/A to wt at base 15)

3023

NH2 3'- C G A G T A C T A G G A T G **T** A G G C -5' CYPwt(-)E3009,19mer,53%GC,Pred Tm=57
NH2 3'-(A)30 C G A G T A C T A G G A T G **T** A G G C -5' CYPwt(-)E3009(A)30-3'NH2
5'- G C T C A T G A T C C T A C **C** T C C G -3' NH2 CYPmut(+)E3009,19mer,58%GC,Pred Tm=59C
5'- G C T C A T G A T C C T A C **C** T C C G (A)30-3' NH2 CYPmut(+)E3009(A)30-3'NH2

|-2998
5'- T G G G G C C T C C T G C T C A T G A T C C T A C A T C C G G A T G T G C A G C|G T G A G C C C A T C -3' Wild Type (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C **C** T C C G G A T G T G C A G C|G T G A G C C C A T C -3' Mut (+)
|-3038-Intron Start

B. CYPwt(-)E3018 (T/C to mut at base 14) and CYPmut(+)E3018 (C/T to wt at base 6)

NH2 3'- G G A T G T A G G C C T A C A C G T C -5' CYPwt(-)E3018,19mer,58%GC, Tm=60
5'- C C T A C A T C C G G A T G T G C A G -3' CYPwt(+)E3018- Target
5'- C C T A C **C** T C C G G A T G T G C A G -3' NH2 CYPmut(+)E3018,19mer, 63%GC, Tm=62C
3'- G G A T G **G** A G G C C T A C A C G T C -5' CYPmut(-)E3018- Target

|-2998
5'- T G G G G C C T C C T G C T C A T G A T C C T A C A T C C G G A T G T G C A G C|G T G A G C C C A T C -3' Wild Type (+)
5'- T G G G G C C T C C T G C T C A T G A T C C T A C **C** T C C G G A T G T G C A G C|G T G A G C C C A T C -3' Mut (+)
|-3038-Intron Start

5. 'G' Allele, CYP2D6*8, $G_{1846}T$, Stop codon, zero enzyme activity

1846

5'- C A C T C C G G T G G G T G A T G G (A)30-3' NH2 CYPwt(+)G1840(A)30-3'NH2,18mer,67%GC, Tm=60
NH2 3'-(A)30 G T G A G G C C A C C C A C T A C C -5' CYPwt(-)G1840(A)30-3'NH2
5'- C A C T C C T G T G G G T G A T G G (A)30-3' NH2 CYPmut(+)G1840(A)30-3'NH2,18mer,61%GC, Tm=57

5'- G T G C C G C C T T C G C C A C T C C|G G T G G G T G A T G G G C A G A A G G G C A C A A A G C G G G -3'
5'- G T G C C G C C T T C G C C A C T C C|T G T G G G T G A T G G G C A G A A G G G C A C A A A G C G G G -3'
Exon 3 end-|-1846

6. "T" Allele, CYP2D6*6, T_{1795} deletion, Frames[redacted]esulting in zero enzyme activity

```
                    5'- G C T G G A G C A G T G G G T G A C -3' NH2          CYPwt(+)T1785,18mer,67%GC, Tm=59-61C
                    5'- G C T G G A G C A G T G G G T G A C (A)30-3' NH2     CYPwt(+)T1785(A)30-3'NH2
                      5'- C T G G A G C A G T G G G T G A C (A)30-3' NH2     CYPwt(+)T1786(A)30-3'NH2
                    5'- G C T G G A G C A G - G G G T G A C -3' NH2          CYPmut(+)T1785,17mer,71%GC, Tm=58-60C
                    5'- G C T G G A G C A G - G G G T G A C (A)30-3' NH2     CYPmut(+)T1785(A)30-3'NH2
                      5'- C T G G A G C A G - G G G T G A C (A)30-3' NH2     CYPmut(+)T1786(A)30-3'NH2
  |-1773
5'- G G G C A A G A A G T C G C T G G A G C A G T G G G T G A C C G A G G A G G C C G C C T G C C T -3'  Wild Type (+)
5'- G G G C A A G A A G T C G C T G G A G C A G - G G G T G A C C G A G G A G G C C G C C T G C C T -3'  Mut (+)
```

7. 2D6/2D7/2D8 Controls - The 2D6/7/8 probes were designed in the 1600 region of the 2D6 gene. The purpose of the designs was to find region somewhere between the PCR primers were it would be easy to discriminate between 2D6 and its two pseudogenes, 2D7 and 2D8. The purpose of the designs is to demonstrate that the PCR amplicon is from the 2D6 gene, not one of the pseudogenes.

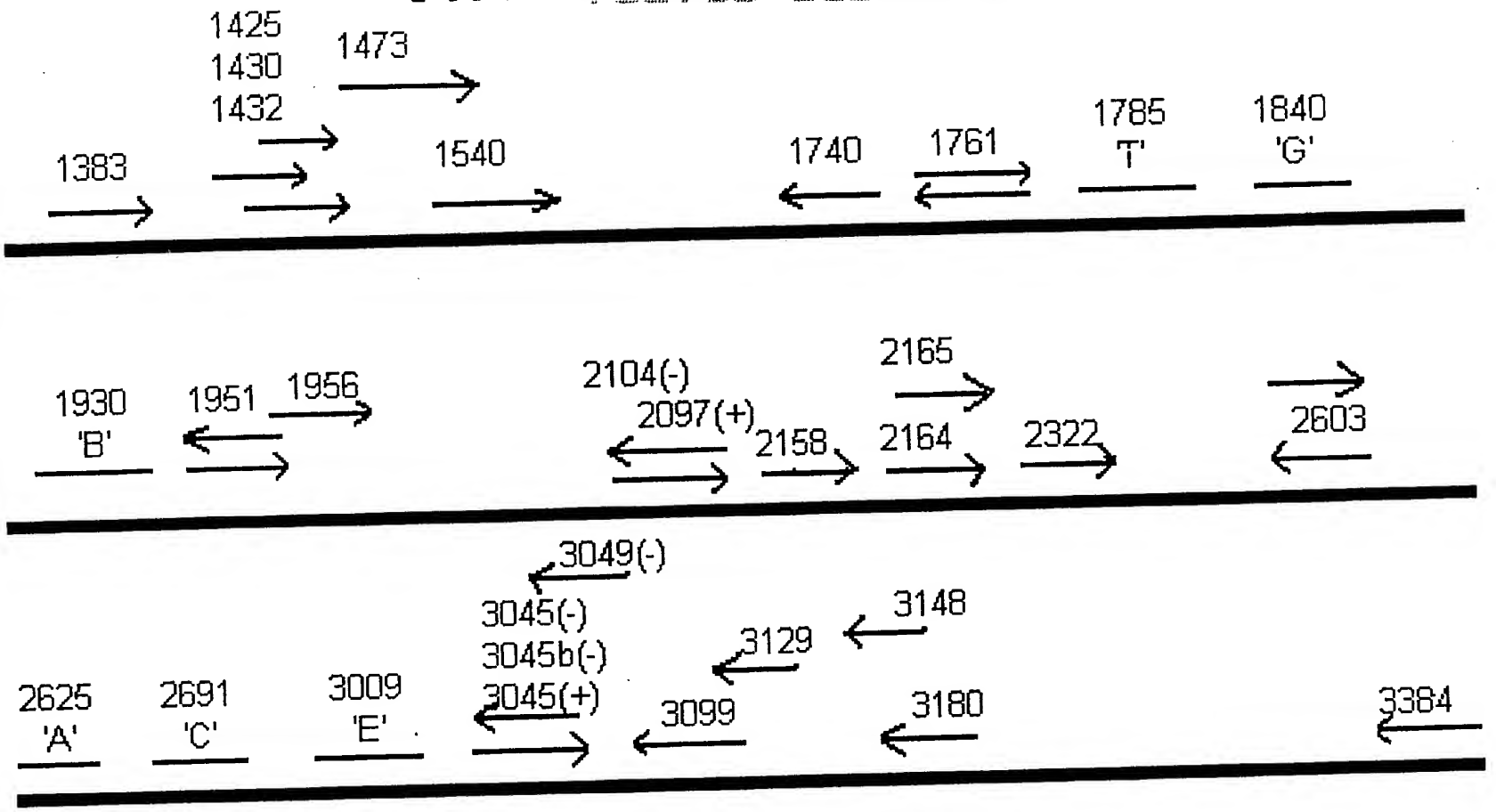
```
                    5'- G A C C A G G G G G A G C - A T A G G (A)30-3' NH2   CYP2D6wt(+)1607(A)30-3'NH2
                    5'- G A C C T T G T G G A G C G C C A G (A)30-3' NH2     CYP2D7wt(+)1607(A)30-3'NH2
                    5'- G A C C A G G A A A A G C - A C A G G (A)30-3' NH2   CYP2D8wt(+)1607(A)30-3'NH2
1603-|              5'- G A C C A G G A A A A G C - A C A G G G (A)30-3' NH2  CYP2D8wt(+)1607b(A)30-3'NH2
  5'-G G G A G A C C A G G G G G A G C - A T A G G G T T G G A G T G G G T G G T -3'  2D6 (+)
  5'-G G G A G A C C T T G T G G A G C G C C A G G G T T G G A G T G G G T G G C -3'  2D7 (+)
  5'-G G G A G A C C A G G A A A A G C - A C A G G G T T G G A G T G G G C G G C -3'  2D8 (+)
```

8. Pos/Neg Control probes- These probes were designed as true positive and negative control probes. They consist of the same semi-random sequence, with the positive control probe having a 5' Biotin.

```
5' Biotin- A T C A T T C C A A T C A T C C A T A T C A T C (A)25-3' NH2   CYP(+)ran(A)25-5'Biotin,3'NH2
    5'- A T C A T T C C A A T C A T C C A T A T C A T C (A)25-3' NH2      CYP(+)ran(A)25-3'NH2
```

Figure 7

CYP2D6 Probes/Primers



CYPwt(+)1383, CYPwt(+)2097, CYPwt(-)2104, and CYPwt(-)3180 are published primer sequences.

1. Chen et al., Clinical Pharmacology and Therapeutics, Vol 60, 5:522-34
2. Heim M, Meyer UA. Lancet 1990; 336:529-32

CYPwt(+)1540 and CYPwt(-)3099 are primers obtained from Intek, referred to as MP3 and MP4 respectively.